

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 09/684,883A
Source: IFW16
Date Processed by STIC: 4/16/07

ENTERED



IFW16

RAW SEQUENCE LISTING DATE: 04/16/2007
PATENT APPLICATION: US/09/684,883A TIME: 19:14:58

Input Set : E:\417c1.app.txt
Output Set: N:\CRF4\04162007\I684883A.raw

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/684,883A

DATE: 04/16/2007
TIME: 19:14:58

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64	10	15	20	
66	gcc aaa ggc ttc agc ccg cgc atc tcc gca ggc tac cgc atc aac gac			316
67	Ala Lys Gly Phe Ser Pro Arg Ile Ser Ala Gly Tyr Arg Ile Asn Asp			
68	25	30	35	
70	ctc cgc ttc gcc gtc gat tac acg ccg tac aaa aac tat aaa gcc cca			364
71	Leu Arg Phe Ala Val Asp Tyr Thr Arg Tyr Lys Asn Tyr Lys Ala Pro			
72	40	45	50	55
74	tcc acc gat ttc aaa ctt tac agc atc ggc gcg tcc gcc att tac gac			412
75	Ser Thr Asp Phe Lys Leu Tyr Ser Ile Gly Ala Ser Ala Ile Tyr Asp			
76	60	65	70	
78	ttc gac acc caa tcg ccc gtc aaa ccg tat ctc ggc gcg cgc ttg agc			460
79	Phe Asp Thr Gln Ser Pro Val Lys Pro Tyr Leu Gly Ala Arg Leu Ser			
80	75	80	85	
82	ctc aac cgc gcc tcc gtc gac ttg ggc ggc agc gac agc ttc agc caa			508
83	Leu Asn Arg Ala Ser Val Asp Leu Gly Gly Ser Asp Ser Phe Ser Gln			
84	90	95	100	
86	acc tcc atc ggc ctc ggc gta ttg acg ggc gta agc tat gcc gtt acc			556
87	Thr Ser Ile Gly Leu Gly Val Leu Thr Gly Val Ser Tyr Ala Val Thr			
88	105	110	115	
90	ccg aat gtc gat ttg gat gcc ggc tac cgc tac aac tac atc ggc aaa			604
91	Pro Asn Val Asp Leu Asp Ala Gly Tyr Arg Tyr Asn Tyr Ile Gly Lys			
92	120	125	130	135
94	gtc aac act gtc aaa aac gtc cgt tcc ggc gaa ctg tcc gtc ggc gtg			652
95	Val Asn Thr Val Lys Asn Val Arg Ser Gly Glu Leu Ser Val Gly Val			
96	140	145	150	
98	cgc gtc aaa ttc tga tatgcgcctt attctgcaaa ccggcgagcc ttccggcggtt			707
99	Arg Val Lys Phe *			
100	155			
102	ttgttttctg ccaccgcaac tacacaaggcc ggccgttttg tacgataatc ccgaatgctg			767
103	cggcttctgc cgccctattt tttgaggaat ccgaaatgtc caaaaaccatc atccacacccg			827
104	aca			830
106	<210> SEQ ID NO: 2			
107	<211> LENGTH: 174			
108	<212> TYPE: PRT			
109	<213> ORGANISM: Neisseria meningitidis			
111	<220> FEATURE:			
112	<221> NAME/KEY: SIGNAL			
113	<222> LOCATION: (1)...(19)			
115	<400> SEQUENCE: 2			
116	Met Lys Lys Ala Leu Ala Thr Leu Ile Ala Leu Ala Leu Pro Ala Ala			
117	-15	-10	-5	
118	Ala Leu Ala Glu Gly Ala Ser Gly Phe Tyr Val Gln Ala Asp Ala Ala			
119	1	5	10	
120	His Ala Lys Ala Ser Ser Ser Leu Gly Ser Ala Lys Gly Phe Ser Pro			
121	15	20	25	
122	Arg Ile Ser Ala Gly Tyr Arg Ile Asn Asp Leu Arg Phe Ala Val Asp			
123	30	35	40	45
124	Tyr Thr Arg Tyr Lys Asn Tyr Lys Ala Pro Ser Thr Asp Phe Lys Leu			
125	50	55	60	

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126 Tyr Ser Ile Gly Ala Ser Ala Ile Tyr Asp Phe Asp Thr Gln Ser Pro
127      65          70          75
128 Val Lys Pro Tyr Leu Gly Ala Arg Leu Ser Leu Asn Arg Ala Ser Val
129      80          85          90
130 Asp Leu Gly Gly Ser Asp Ser Phe Ser Gln Thr Ser Ile Gly Leu Gly
131      95         100         105
132 Val Leu Thr Gly Val Ser Tyr Ala Val Thr Pro Asn Val Asp Leu Asp
133 110        115        120        125
134 Ala Gly Tyr Arg Tyr Asn Tyr Ile Gly Lys Val Asn Thr Val Lys Asn
135           130        135        140
136 Val Arg Ser Gly Glu Leu Ser Val Gly Val Arg Val Lys Phe
137           145        150        155
140 <210> SEQ ID NO: 3
141 <211> LENGTH: 710
142 <212> TYPE: DNA
143 <213> ORGANISM: Neisseria meningitidis
145 <220> FEATURE:
146 <221> NAME/KEY: CDS
147 <222> LOCATION: (116) ... (643)
149 <220> FEATURE:
150 <221> NAME/KEY: sig_peptide
151 <222> LOCATION: (116) ... (172)
153 <220> FEATURE:
154 <221> NAME/KEY: mat_peptide
155 <222> LOCATION: (173) ... (643)
157 <400> SEQUENCE: 3
158 gtatctttag gcattgaaaa tattacaatg caaaaagaaa atttcagtat aatacggcag 60
159 gattcttaa cggttttta accattttc tccctgacca taaaggaatc aagat atg 118
160                               Met
163 aaa aaa gca ctt gcc gca ctg att gcc ctc gcc ctc ccg gcc gca 166
164 Lys Lys Ala Leu Ala Ala Leu Ile Ala Leu Ala Leu Pro Ala Ala Ala
165       -15        -10        -5
167 ctg gcg gaa ggc gca tcc ggc ttt tac gtc caa gcc gat gcc gca cac 214
168 Leu Ala Glu Gly Ala Ser Gly Phe Tyr Val Gln Ala Asp Ala Ala His
169       1          5          10
171 gcc aaa gcc tca agc tct tta ggt tct gcc aaa ggc ttc agc ccg cgc 262
172 Ala Lys Ala Ser Ser Ser Leu Gly Ser Ala Lys Gly Phe Ser Pro Arg
173   15        20        25        30
175 atc tcc gca ggc tac cgc atc aac gac ctc cgc ttc gcc gtc gat tac 310
176 Ile Ser Ala Gly Tyr Arg Ile Asn Asp Leu Arg Phe Ala Val Asp Tyr
177       35        40        45
179 acg cgc tac aaa aac tat aaa caa gtc cca tcc acc gat ttc aaa ctt 358
180 Thr Arg Tyr Lys Asn Tyr Lys Gln Val Pro Ser Thr Asp Phe Lys Leu
181       50        55        60
183 tac agc atc ggc gcg tcc gcc att tac gac ttc gac acc caa tcc ccc 406
184 Tyr Ser Ile Gly Ala Ser Ala Ile Tyr Asp Phe Asp Thr Gln Ser Pro
185       65        70        75
187 gtc aaa ccg tat ctc ggc gcg cgc ttg agc ctc aac cgc gcc tcc gtc 454
188 Val Lys Pro Tyr Leu Gly Ala Arg Leu Ser Leu Asn Arg Ala Ser Val

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189	80	85	90	
191	gac ttt aac ggc agc gac agc ttc agc caa acc tcc acc ggc ctc ggc			502
192	Asp Phe Asn Gly Ser Asp Ser Phe Ser Gln Thr Ser Thr Gly Leu Gly			
193	95	100	105	110
195	gta ttg gcg ggc gta agc tat gcc gtt acc ccg aat gtc gat ttg gat			550
196	Val Leu Ala Gly Val Ser Tyr Ala Val Thr Pro Asn Val Asp Leu Asp			
197	115	120	125	
199	gcc ggc tac cgc tac aac tac atc ggc aaa gtc aac act gtc aaa aat			598
200	Ala Gly Tyr Arg Tyr Asn Tyr Ile Gly Lys Val Asn Thr Val Lys Asn			
201	130	135	140	
203	gtc cgt tcc ggc gaa ctg tcc ggc gta cgc gtc aaa ttc tga			643
204	Val Arg Ser Gly Glu Leu Ser Ala Gly Val Arg Val Lys Phe *			
205	145	150	155	
207	tatacgcgtt attccgcaaa ccggccgagcc ttccggcggt ttgtttcc gcccggcaaa			703
208	ctacaca			710
210	<210> SEQ ID NO: 4			
211	<211> LENGTH: 175			
212	<212> TYPE: PRT			
213	<213> ORGANISM: Neisseria meningitidis			
215	<220> FEATURE:			
216	<221> NAME/KEY: SIGNAL			
217	<222> LOCATION: (1)...(19)			
219	<400> SEQUENCE: 4			
220	Met Lys Lys Ala Leu Ala Ala Leu Ile Ala Leu Ala Leu Pro Ala Ala			
221	-15	-10	-5	
222	Ala Leu Ala Glu Gly Ala Ser Gly Phe Tyr Val Gln Ala Asp Ala Ala			
223	1	5	10	
224	His Ala Lys Ala Ser Ser Ser Leu Gly Ser Ala Lys Gly Phe Ser Pro			
225	15	20	25	
226	Arg Ile Ser Ala Gly Tyr Arg Ile Asn Asp Leu Arg Phe Ala Val Asp			
227	30	35	40	45
228	Tyr Thr Arg Tyr Lys Asn Tyr Lys Gln Val Pro Ser Thr Asp Phe Lys			
229	50	55	60	
230	Leu Tyr Ser Ile Gly Ala Ser Ala Ile Tyr Asp Phe Asp Thr Gln Ser			
231	65	70	75	
232	Pro Val Lys Pro Tyr Leu Gly Ala Arg Leu Ser Leu Asn Arg Ala Ser			
233	80	85	90	
234	Val Asp Phe Asn Gly Ser Asp Ser Phe Ser Gln Thr Ser Thr Gly Leu			
235	95	100	105	
236	Gly Val Leu Ala Gly Val Ser Tyr Ala Val Thr Pro Asn Val Asp Leu			
237	110	115	120	125
238	Asp Ala Gly Tyr Arg Tyr Asn Tyr Ile Gly Lys Val Asn Thr Val Lys			
239	130	135	140	
240	Asn Val Arg Ser Gly Glu Leu Ser Ala Gly Val Arg Val Lys Phe			
241	145	150	155	
244	<210> SEQ ID NO: 5			
245	<211> LENGTH: 850			
246	<212> TYPE: DNA			
247	<213> ORGANISM: Neisseria meningitidis			

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249 <220> FEATURE:
 250 <221> NAME/KEY: CDS
 251 <222> LOCATION: (208)...(732)
 253 <220> FEATURE:
 254 <221> NAME/KEY: sig_peptide
 255 <222> LOCATION: (208)...(264)
 257 <220> FEATURE:
 258 <221> NAME/KEY: mat_peptide
 259 <222> LOCATION: (265)...(732)
 261 <400> SEQUENCE: 5
 262 cacccatccg ccgcgtatcg cggccaccac cattaaagg caacgcgcgg gttaacggct 60
 263 ttgccgtcg aaagcagcc ggataccgct acgtatctt aagtattaaa aatattacga 120
 264 tgcaaaaaga aaatttaagt ataataaagc agaattctt aacggattct taacaatttt 180
 265 tctaactgac cataaaggaa ccaaat atg aaa aaa gca ctt gcc aca ctg att 234
 266 Met Lys Lys Ala Leu Ala Thr Leu Ile
 267 -15
 269 gcc ctc gct ctc ccg gcc gca ctg gcg gaa ggc gca tcc ggc ttt 282
 270 Ala Leu Ala Leu Pro Ala Ala Ala Leu Ala Glu Gly Ala Ser Gly Phe
 271 -10 -5 1 5
 273 tac gtc caa gcc gat gcc gca cac gca aaa gcc tca agc tct tta ggt 330
 274 Tyr Val Gln Ala Asp Ala Ala His Ala Lys Ala Ser Ser Ser Leu Gly
 275 10 15 20
 277 tct gcc aaa ggc ttc agc ccg cgc atc tcc gca ggc tac cgc atc aac 378
 278 Ser Ala Lys Gly Phe Ser Pro Arg Ile Ser Ala Gly Tyr Arg Ile Asn
 279 25 30 35
 281 gac ctc cgc ttc gcc gtc gat tac acg cgc tac aaa aac tat aaa gcc 426
 282 Asp Leu Arg Phe Ala Val Asp Tyr Thr Arg Tyr Lys Asn Tyr Lys Ala
 283 40 45 50
 285 cca tcc acc gat ttc aaa ctt tac agc atc ggc gcg tcc gcc att tac 474
 286 Pro Ser Thr Asp Phe Lys Leu Tyr Ser Ile Gly Ala Ser Ala Ile Tyr
 287 55 60 65 70
 289 gac ttc gac acc caa tcg ccc gtc aaa ccg tat ctc ggc gcg cgc ttg 522
 290 Asp Phe Asp Thr Gln Ser Pro Val Lys Pro Tyr Leu Gly Ala Arg Leu
 291 75 80 85
 293 agc ctc aac cgc gcc tcc gtc gac ttg ggc ggc agc gac agc ttc agc 570
 294 Ser Leu Asn Arg Ala Ser Val Asp Leu Gly Gly Ser Asp Ser Phe Ser
 295 90 95 100
 297 caa acc tcc acc ggc ctc ggc gta ttg gcg ggc gta agc tat gcc gtt 618
 298 Gln Thr Ser Thr Gly Leu Gly Val Leu Ala Gly Val Ser Tyr Ala Val
 299 105 110 115
 301 acc ccg aat gtc gat ttg gat gcc ggc tac cgc tac aac tac atc ggc 666
 302 Thr Pro Asn Val Asp Leu Asp Ala Gly Tyr Arg Tyr Asn Tyr Ile Gly
 303 120 125 130
 305 aaa gtc aac act gtc aaa aac gtc cgt tcc ggc gaa ctg tcc gcc ggt 714
 306 Lys Val Asn Thr Val Lys Asn Val Arg Ser Gly Glu Leu Ser Ala Gly
 307 135 140 145 150
 309 gtg cgc gtc aaa ttc tga tatgcgcctt attctgcaaa cggccgagcc 762
 310 Val Arg Val Lys Phe *
 311 155

RAW SEQUENCE LISTING ERROR SUMMARY DATE: 04/16/2007
PATENT APPLICATION: US/09/684,883A TIME: 19:14:59

FYI
Input Set : E:\417c1.app.txt
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:30; Xaa Pos. 7,73,126

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/684,883A

DATE: 04/16/2007

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Input Set : E:\417c1.app.txt

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L:689 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:30 after pos.:0

M:341 Repeated in SeqNo=30